

## THE STUDY OF POLYMORPHISM OF TGF-BETA1 IN PATIENTS WITH CIRRHOSIS CAUSED BY CHRONIC HEPATITIS C

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TGF $\beta$ 1 along with PDGF, VEGF, Angiotensin II, MCP-1, TNF, belongs to peptide ligands, which reinforce of signal transduction of fibrogenesis. TGF $\beta$ 1 operates through receptor serine/threonine kinase and involves Smads and Src kinases. The aim of the present study was to identify potential markers of cytokines genes associated with the susceptibility to HCV infection.

**Material and methods:** This prospective study was performed on 120 patients having chronic hepatitis C, 53 of them are women and 67 are men, and on healthy donors 70 people. Patients were divided into groups: 1 group - with chronic hepatitis C without cirrhosis - 40 people, 2 group - with cirrhosis in the outcome of hepatitis C Class A (Child-Pugh) - 35 people and group 3 with diagnosis of cirrhosis Class B and C - 45

**Results:** The results of the study of polymorphism of TGF- $\beta$ 1 in patients with hepatitis C showed that clinically significant chronic HCV infection in the Kazakh population is associated with homozygous inheritance of the G allele of the 25 codon of the TGF $\beta$ 1 gene. The development of cirrhosis is associated with the more frequent inheritance of the GG 25 homozygous genotype of the (P < 0.05).

**Conclusion:** The functionally relevant TGF- $\beta$ 1 polymorphism may play a role in the clinically significant chronic HCV infection in the Kazakh population. In chronic hepatitis C, there is a significantly low incidence of the allele C of the 25 codon of the TGF $\beta$ 1 gene. The development of hepatic cirrhosis is associated with a more frequent inheritance of the homozygous genotype GG 25 of the codon of the TGF $\beta$ 1 gene.